SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 50 .

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds
                                               (without alignments)
                                               572.596 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: .19
Sequence: 1 gcagaatggtgacgctaat 19

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4107832S seqs, 2339354122B residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_est3:*
                4: gb_htc:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_est7:*
                9: gb_gss1:*
                10: gb_gss2:*
                11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

Result Query
No.   Score Match Length DB ID   Description

No matches found

Search completed: February 5, 2006, 13:07:28
Job time : 1552.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds
                                             (without alignments)
                                             1208.082 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: 19
Sequence: 1 gcagaatggtgacgctaat 19

Scoring table: OLIGO_NUC
                Gapop_60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pr:*
                 9: gb_ro:*
                10: gb_sts:*
                11: gb_sy:*
                12: gb_un:*
                13: gb_vi:*
                14: gb_htg:*
                15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result   Query
No.   Score Match Length DB ID   Description
------ ----- ----- ------ -- --   -----------

No matches found

Search completed: February 5, 2006, 12:01:29
Job time : 894 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 07:35:28 ; Search time 218.5 Seconds
(without alignments)
579.538 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: 19
Sequence: 1 gcagaatggtgacgctaat 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 333246308 residues
Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	13	ADT26144	Adt26144 siRNA C f

ALIGNMENTS

RESULT 1
ADT26144
ID   ADT26144 standard; RNA; 19 BP.
XX
AC   ADT26144;
XX
DT   27-JAN-2005 (first entry)
XX
DE   siRNA C for potassium channel subunit Kv3.4.
XX
KW   RNA interference; gene silencing; ds; potassium channel;
KW   fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;
KW   siRNA; small interfering RNA; neurological condition; epilepsy; hearing;
KW   learning and memory disorder.
XX
OS   Rattus rattus.
XX
PN   US2004220082-A1.
XX
PD   04-NOV-2004.
XX
PF   21-JAN-2004; 2004US-00761557.
XX
PR   21-JAN-2003; 2003US-0441375P.
XX
PA   (NOUN) UNIV NORTHWESTERN.
XX
PI   Surmeier DJ, Tkatch T, Baranauskas G;
XX
DR   WPI; 2004-774947/76.
XX
PT   Inhibiting the ability of a fast-spiking neuronal cell to discharge at a
PT   high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's
PT   disease and other neurological conditions.
XX
PS   Example 6; SEQ ID NO 3; 27pp; English.
XX
CC   The invention relates to inhibiting the ability of a fast-spiking
CC   neuronal cell to discharge at a high rate comprising providing a compound
CC   capable of inhibiting Kv3.4 activity (potassium channel subunit) to a
CC   cell expressing Kv3 channels comprising a Kv3.4 subunit (especially the
CC   Kv3.4a subunit), where the high rate of discharge is inhibited. Also
CC   included are a method of manipulating neuronal ion channels (comprising
CC   transfecting a fast-spiking neuronal cell with a vector encoding an siRNA
CC   (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein
CC   where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a
CC   composition comprising an siRNA construct capable of inhibiting
CC   expression of a Kv3.4 subunit in a neuronal cell and a method for
CC   screening for compounds that inhibit the activity of a Kv3.4 protein
CC   (comprising providing a cell expressing Kv3.4 protein, and a test
CC   compound, and detecting the activity of the Kv3.4 protein in the presence
CC   of the test compound). The method id useful for manipulating ion
CC   channels, in particular for treating Parkinson's disease and other
CC   neurological conditions, such as epilepsy, hearing, learning and memory
CC   disorders. The present sequence is an siRNA targeting nucleotides 1626-
CC   1644 (relative to the start codon) of the rat Kv3.4 mRNA.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match   100.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCAGAATGGTGACGCTAAT 19
          |||||||||||||||||||
Db   1 GCAGAATGGTGACGCTAAT 19

Search completed: February   5, 2006, 11:31:35
Job time : 218.5 secs

us-10-761-557-3.rni

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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds
                                              (without alignments)
                                              469.079 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: 19
Sequence: 1 gcagaatggtgacgctaat 19

Scoring table: OLIGO_NUC
                 Gapop_60.0 , Gapext 60.0

Searched: 1303057 seqs, 88878028 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   Issued Patents NA:*
                 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

                                          SUMMARIES

                 %
Result   Query
No. Score Match Length DB ID   Description

No matches found

Search completed: February 5, 2006, 12:04:00
Job time : 72 secs

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2006  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       February  5, 2006, 11:21:57 ; Search time 344.5 Seconds
                                           (without alignments)
                                  456.076 Million cell updates/sec

Title:          US-10-761-557-3
Perfect score:  19
Sequence:       1 gcagaatggtgacgctaat 19

Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       9793542 seqs, 413468905 residues

Word size :     19

Total number of hits satisfying chosen parameters:      1

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :      Published Applications NA Main:*
                1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                3:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                4:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                5:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                6:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                7:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                8:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                9:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
               10:  /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.


                          SUMMARIES

                %
Result    Query
No.   Score Match Length DB ID                     Description
----- ----- ----- ------ -- ---------------- ---------------------
  1     19  100.0   19    8 US-10-761-557-3    Sequence 3, Appli


                         ALIGNMENTS


RESULT 1
US-10-761-557-3
; Sequence 3, Application US/10761557
; Publication No. US20040220082A1
; GENERAL INFORMATION:
;  APPLICANT: Surmeier, D. James
;  APPLICANT: Tkatch, Tatiana
;  APPLICANT: Baranauskas, Gytis
;  TITLE OF INVENTION: Manipulation of Neuronal Ion Channels
;  FILE REFERENCE: NWESTERN-08739
;  CURRENT APPLICATION NUMBER: US/10/761,557
;  CURRENT FILING DATE:  2004-01-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;  LENGTH: 19
;  TYPE: DNA
```

```
; ORGANISM: Rattus rattus
US-10-761-557-3

Query Match            100.0%;  Score 19;  DB 8;  Length 19;
Best Local Similarity  100.0%;  Pred. No. 0.16;
Matches  19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy      1 GCAGAATGGTGACGCTAAT 19
          |||||||||||||||||||
Db      1 GCAGAATGGTGACGCTAAT 19

Search completed: February  5, 2006, 12:15:36
Job time : 344.5 secs
```

OM nucleic - nucleic search, using sw model

Copyright   GenCore version 5.1.6
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Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds
                                            (without alignments)
                                        86.540 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: 19
Sequence: 1 gcagaatggtgacgctaat 19

Scoring table: OLIGO_NUC
                Gapop_60.0 , Gapext 60.0

Searched: 6068529 seqs, 41903697 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   Published Applications NA New:*
                1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
                8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
               10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
               11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

          %
Result   Query
No.   Score Match Length DB ID   Description
----- --   -----------

No matches found

Search completed: February 5, 2006, 13:13:41
Job time : 184 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds
                                              (without alignments)
                                              572.596 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggcagtgttgagccgaaac 19

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339354l228 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   EST:*
                  1: gb_est1:*
                  2: gb_est2:*
                  3: gb_est3:*
                  4: gb_htc:*
                  5: gb_est4:*
                  6: gb_est5:*
                  7: gb_est6:*
                  8: gb_est7:*
                  9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

                              %
Result   Query
No.   Score   Match Length DB ID   Description

No matches found

Search completed: February 5, 2006, 13:07:28
Job time : 1552.5 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds
                                             (without alignments)
                                             1208.082 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggcagtgttgagccgaaac 19

Scoring table: OLIGO_NUC
                  Gapop_60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   GenEmbl:*
                   1: gb_ba:*
                   2: gb_in:*
                   3: gb_env:*
                   4: gb_om:*
                   5: gb_ov:*
                   6: gb_pat:*
                   7: gb_ph:*
                   8: gb_pr:*
                   9: gb_ro:*
                  10: gb_sts:*
                  11: gb_sy:*
                  12: gb_un:*
                  13: gb_vi:*
                  14: gb_htg:*
                  15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

                                          %
Result   Query
  No. Score Match Length DB ID   Description

No matches found

Search completed: February 5, 2006, 12:01:29
Job time : 894 secs

```
                GenCore version 5.1.6
          Copyright (c) 1993 - 2006 Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:      February 5, 2006, 07:35:28 ; Search time 218.5 Seconds
                                           (without alignments)
                                           579.538 Million cell updates/sec

Title:          US-10-761-557-4
Perfect score:  19
Sequence:       1 ggcagtgttgagccgaaac 19

Scoring table:  OLIGO NUC
                Gapop 60.0 , Gapext 60.0

Searched:       4996997 seqs, 333234308 residues
Word size :     19

Total number of hits satisfying chosen parameters:        1

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :      N_Geneseq_21:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	Length	ID	Description
1	19	100.0	19	13	ADT26145		Adt26145 siRNA D f

```
                        ALIGNMENTS

RESULT 1
ADT26145
ID   ADT26145 standard; RNA; 19 BP.
XX
AC   ADT26145;
XX
DT   27-JAN-2005  (first entry)
XX
DE   siRNA D for potassium channel subunit Kv3.4.
XX
KW   RNA interference; gene silencing; ds; potassium channel;
KW   fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;
KW   siRNA; small interfering RNA; neurological condition; epilepsy; hearing;
KW   learning and memory disorder.
XX
OS   Rattus rattus.
XX
PN   US2004220082-A1.
XX
PD   04-NOV-2004.
XX
PF   21-JAN-2004; 2004US-00761557.
XX
PR   21-JAN-2003; 2003US-0441375P.
XX
PA   (NOUN ) UNIV NORTHWESTERN.
XX
PI   Surmeier DJ, Tkatch T, Baranauskas G;
XX
DR   WPI; 2004-774947/76.
XX
PT   Inhibiting the ability of a fast-spiking neuronal cell to discharge at a
PT   high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's
PT   disease and other neurological conditions.
XX
PS   Example 6; SEQ ID NO 4; 27pp; English.
XX
CC   The invention relates to inhibiting the ability of a fast-spiking
CC   neuronal cell to discharge at a high rate comprising providing a compound
CC   capable of inhibiting Kv3.4 activity (potassium channel subunit) to a
CC   cell expressing Kv3 channels comprising a Kv3.4 subunit (especially the
CC   Kv3.4a subunit), where the high rate of discharge is inhibited. Also
CC   included are a method of manipulating neuronal ion channels (comprising
CC   transfecting a fast-spiking neuronal cell with a vector encoding an siRNA
CC   (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein
CC   where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a
CC   composition comprising an siRNA construct capable of inhibiting
CC   expression of a Kv3.4 subunit in a neuronal cell and a method for
CC   screening for compounds that inhibit the activity of a Kv3.4 protein
CC   (comprising providing a cell expressing Kv3.4 protein, and a test
CC   compound, and detecting the activity of the Kv3.4 protein in the presence
CC   of the test compound). The method id useful for manipulating ion
CC   channels, in particular for treating Parkinson's disease and other
CC   neurological conditions, such as epilepsy, hearing, learning and memory
CC   disorders. The present sequence is an siRNA targeting nucleotides 11825-
CC   1843 (relative to the start codon) of the rat Kv3.4 mRNA.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match             100.0%;  Score 19;  DB 13;  Length 19;
Best Local Similarity   100.0%;  Pred. No. 0.16;
Matches   19;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 GGCAGTGTTGAGCCGAAAC 19
              |||||||||||||||||||
Db          1 GGCAGTGTTGAGCCGAAAC 19


Search completed: February  5, 2006, 11:31:35
Job time : 218.5 secs
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds
                                              (without alignments)
                                              469.079 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggcagtgttgagccgaaac 19

Scoring table: OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 88878O828 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :   Issued Patents NA:*
                  1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                  8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                  9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   %
 No.   Score   Query   Match Length DB ID   Description

No matches found

Search completed: February 5, 2006, 12:04:00
Job time : 72 secs

OM nucleic - nucleic search, using sw model

```
          GenCore version 5.1.6
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Run on:    February  5, 2006, 11:21:57 ; Search time 344.5 Seconds
                                         (without alignments)
                                         456.076 Million cell updates/sec

Title:          US-10-761-557-4
Perfect score:  19
Sequence:       1 ggcagtgttgagccgaaac 19

Scoring table:  OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched:       9793542 seqs, 413468905 residues

Word size :     19

Total number of hits satisfying chosen parameters:    1

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :    Published Applications_NA_Main:*
        1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
        2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
        3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
        4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
        5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
        6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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                          SUMMARIES

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No.    Score  Match Length DB ID                Description
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                          ALIGNMENTS

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; Sequence 4, Application US/10761557
; Publication No. US20040220082A1
; GENERAL INFORMATION:
;  APPLICANT: Surmeier, D. James
;  APPLICANT: Tkatch, Tatiana
;  APPLICANT: Baranauskas, Gytis
;  TITLE OF INVENTION: Manipulation of Neuronal Ion Channels
;  FILE REFERENCE: NWESTERN-08739
;  CURRENT APPLICATION NUMBER: US/10/761,557
;  CURRENT FILING DATE: 2004-01-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;  LENGTH: 19
;  TYPE: DNA
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; ORGANISM: Rattus rattus
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Best Local Similarity 100.0%;  Pred. No. 0.059;
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Job time : 344.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds
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                                          86.540 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggcagtgtgagccgaaac 19

Scoring table: OLIGO NUC
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Searched: 6068529 seqs, 419036697 residues

Word size :   19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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Result   Query
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No matches found

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DEFINITION  R.rattus mRNA for potassium channel protein (2858 bp).
ACCESSION   X62841
VERSION     X62841.1  GI:57648
KEYWORDS    voltage-gated potassium channel.
SOURCE      Rattus rattus (black rat)
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            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 2858)
  AUTHORS   Retting,J., Wunder,F., Stocker,M., Lichtinghagen,R., Mastiaux,F.,
            Beckh,S., Kues,W., Pedarzani,P., Schroeter,K.H., Ruppersberg,J.P.,
            Veh,R. and Pongs,O.
  TITLE     Characterization of a Shaw-related potassium channel family in rat
            brain
  JOURNAL   EMBO J. 11 (7), 2473-2486 (1992)
   PUBMED   1378392
REFERENCE   2  (bases 1 to 2858)
  AUTHORS   Pongs,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1991) O. Pongs, Zentrum f Molekulare
            Neurobiologie, ZMNH Haus 42, Martinistr 52, 2000 Hamburg 20, FRG
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; DEFINITION  R.rattus mRNA for potassium channel protein (2858 bp).
; ACCESSION   X62841
; VERSION     X62841.1  GI:57648
; KEYWORDS    voltage-gated potassium channel.
; SOURCE      Rattus rattus (black rat)
; ORGANISM    Rattus rattus
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
;             Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
; REFERENCE   1  (bases 1 to 2858)
; AUTHORS     Retting,J., Wunder,F., Stocker,M., Lichtinghagen,R., Mastiaux,F.,
;             Beckh,S., Kues,W., Pedarzani,P., Schroeter,K.H., Ruppersberg,J.P.,
;             Veh,R. and Pongs,O.
; TITLE       Characterization of a Shaw-related potassium channel family in rat
;             brain
; JOURNAL     EMBO J. 11 (7), 2473-2486 (1992)
; PUBMED      1378392
; REFERENCE   2  (bases 1 to 2858)
; AUTHORS     Pongs,O.
; TITLE       Direct Submission
; JOURNAL     Submitted (22-OCT-1991) O. Pongs, Zentrum f Molekulare
;             Neurobiologie, ZMNH Haus 42, Martinistr 52, 2000 Hamburg 20, FRG
; FEATURES             Location/Qualifiers
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